

Does Not Comply
Corrected Diskette Needed

see page 8



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/925,576B

DATE: 07/15/2002

TIME: 09:11:12

Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\07152002\I925576B.raw

3 <110> APPLICANT: Andersen, Carsten
4 Borchert, Torben Vedel
5 Nielsen, Bjarne Ronfeldt
7 <120> TITLE OF INVENTION: Amylase Variants
9 <130> FILE REFERENCE: 10004.204-US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/925,576B
C--> 11 <141> CURRENT FILING DATE: 2001-08-09
E--> 11 <160> NUMBER OF SEQ ID NOS: 20
13 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

283 <210> SEQ ID NO: 3
284 <211> LENGTH: 1455
285 <212> TYPE: DNA
286 <213> ORGANISM: Bacillus sp.
288 <220> FEATURE:
289 <221> NAME/KEY: CDS
290 <222> LOCATION: (1)..(1455)
291 <223> OTHER INFORMATION: SP722
294 <400> SEQUENCE: 3
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296 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
297 1 5 10 15
299 ttg cct aat gat ggg aat cac tgg aat aga tta aga gat gat gct agt 96
300 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
301 20 25 30
303 aat cta aga aat aga ggt ata acc gct att tgg att ccg cct gcc tgg 144
304 Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
E--> 305 35
W--> 307 <110> APPLICANT: Andersen, Carsten
W--> 307 <110> APPLICANT: Andersen, Carsten
W--> 311 <120> TITLE OF INVENTION: Amylase Variants
W--> 311 <120> TITLE OF INVENTION: Amylase Variants
W--> 313 <130> FILE REFERENCE: 10004.204-US
W--> 313 <130> FILE REFERENCE: 10004.204-US
W--> 315 <160> NUMBER OF SEQ ID NOS: 20
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W--> 317 <170> SOFTWARE: PatentIn version 3.1
319 <210> SEQ ID NO: 1
320 <211> LENGTH: 1455
321 <212> TYPE: DNA

SEQUENCE LISTING

remove repeated material

RAW SEQUENCE LISTING

DATE: 07/15/2002

PATENT APPLICATION: US/09/925,576B

TIME: 09:11:12

Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\07152002\I925576B.raw

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322 <213> ORGANISM: Bacillus sp.
324 <220> FEATURE:
325 <221> NAME/KEY: CDS
326 <222> LOCATION: (1)..(1455)
327 <223> OTHER INFORMATION: SP690
330 <400> SEQUENCE: 1
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332 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
333 1          5          10          15
335 ttg cca aat gac ggg aat cat tgg aac agg ttg agg gat gac gca gct      96
336 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
337          20          25          30
339 aac tta aag agt aaa ggg ata aca gct gta tgg atc cca cct gca tgg      144
340 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
341          35          40          45
343 aag ggg act tcc cag aat gat gta ggt tat gga gcc tat gat tta tat      192
344 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
345          50          55          60
347 gat ctt gga gag ttt aac cag aag ggg acg gtt cgt aca aaa tat gga      240
348 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
349 65          70          75          80
351 aca cgc aac cag cta cag gct gcg gtg acc tct tta aaa aat aac ggc      288
352 Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
353          85          90          95
355 att cag gta tat ggt gat gtc gtc atg aat cat aaa ggt gga gca gat      336
356 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
357          100          105          110
359 ggt acg gaa att gta aat gcg gta gaa gtg aat cgg agc aac cga aac      384
360 Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
361          115          120          125
363 cag gaa acc tca gga gag tat gca ata gaa gcg tgg aca aag ttt gat      432
364 Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
365          130          135          140
367 ttt cct gga aga gga aat aac cat tcc agc ttt aag tgg cgc tgg tat      480
368 Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
369 145          150          155          160
371 cat ttt gat ggg aca gat tgg gat cag tca cgc cag ctt caa aac aaa      528
372 His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
373          165          170          175
375 ata tat aaa ttc agg gga aca ggc aag gcc tgg gac tgg gaa gtc gat      576
376 Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
377          180          185          190
379 aca gag aat ggc aac tat gac tat ctt atg tat gca gac gtg gat atg      624
380 Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
381          195          200          205
383 gat cac cca gaa gta ata cat gaa ctt aga aac tgg gga gtg tgg tat      672
384 Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
385          210          215          220
387 acg aat aca ctg aac ctt gat gga ttt aga ata gat gca gtg aaa cat      720

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*remove
repeated
material*

RAW SEQUENCE LISTING

DATE: 07/15/2002

PATENT APPLICATION: US/09/925,576B

TIME: 09:11:12

Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\07152002\I925576B.raw

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388 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
389 225                230                235                240
391 ata aaa tat agc ttt acg aga gat tgg ctt aca cat gtg cgt aac acc      768
392 Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
393                245                250                255
395 aca ggt aaa cda atg ttt gca gtg gct gag ttt tgg aaa aat gac ctt      816
W--> 396 Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn gaa tca ttt gta caa gaa
E--> 397 tgg ttt aag cca ctt gct      1056
398 Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
W--> 399                340                345                350
E--> 401 tat gcg ctt att tta aca aga gaa caa ggc tat ccc tct gtc ttc tat      1104
402 Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
W--> 403                355                360                365
E--> 405 ggt gac tac tat gga att cca aca cat agt gtc cca gca atg aaa gcc      1152
406 Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
W--> 407                370                375                380
E--> 409 aag att gat cca atc tta gag gcg cgt caa aat ttt gca tat gga aca      1200
410 Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
W--> 411 385                390                395                400
E--> 413 caa cat gat tat ttt gac cat cat aat ata atc gga tgg aca cgt gaa      1248
414 Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
W--> 415                405                410                415
E--> 417 gga aat acc acg cat ccc aat tca gga ctt gcg act atc atg tcg gat      1296
418 Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
W--> 419                420                425                430
E--> 421 ggg cca ggg gga gag aaa tgg atg tac gta ggg caa aat aaa gca ggt      1344
422 Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
W--> 423                435                440                445
E--> 425 caa gtt tgg cat gac ata act gga aat aaa cca gga aca gtt acg atc      1392
426 Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
W--> 427                450                455                460
E--> 429 aat gca gat gga tgg gct aat ttt tca gta aat gga gga tct gtt tcc      1440
430 Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
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E--> 435                485
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570 <211> LENGTH: 1548
571 <212> TYPE: DNA
572 <213> ORGANISM: Bacillus stearothermophilus
574 <220> FEATURE:
575 <221> NAME/KEY: CDS
576 <222> LOCATION: (1)..(1548)
577 <223> OTHER INFORMATION: BSG
580 <400> SEQUENCE: 5
581 gcc gca ccg ttt aac ggc acc atg atg cag tat ttt gaa tgg tac ttg      48
582 Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu

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*Remove
repeated
material*

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Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\07152002\I925576B.raw

583	1				5					10					15					
585	ccg	gat	gat	ggc	acg	tta	tgg	acc	aaa	gtg	gcc	aat	gaa	gcc	aac	aac				96
586	Pro	Asp	Asp	Gly	Thr	Leu	Trp	Thr	Lys	Val	Ala	Asn	Glu	Ala	Asn	Asn				
587				20					25					30						
589	tta	tcc	agc	ctt	ggc	atc	acc	gct	ctt	tgg	ctg	ccg	ccc	gct	tac	aaa				144
590	Leu	Ser	Ser	Leu	Gly	Ile	Thr	Ala	Leu	Trp	Leu	Pro	Pro	Ala	Tyr	Lys				
591			35					40					45							
593	gga	aca	agc	cgc	agc	gac	gta	ggg	tac	gga	gta	tac	gac	ttg	tat	gac				192
594	Gly	Thr	Ser	Arg	Ser	Asp	Val	Gly	Tyr	Gly	Val	Tyr	Asp	Leu	Tyr	Asp				
595		50					55					60								
597	ctc	ggc	gaa	ttc	aat	caa	aaa	ggg	acc	gtc	cgc	aca	aaa	tac	gga	aca				240
598	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr				
599	65					70					75					80				
601	aaa	gct	caa	tat	ctt	caa	gcc	att	caa	gcc	gcc	cac	gcc	gct	gga	atg				288
602	Lys	Ala	Gln	Tyr	Leu	Gln	Ala	Ile	Gln	Ala	Ala	His	Ala	Ala	Gly	Met				
603					85				90						95					
605	caa	gtg	tac	gcc	gat	gtc	gtg	ttc	gac	cat	aaa	ggc	ggc	gct	gac	ggc				336
606	Gln	Val	Tyr	Ala	Asp	Val	Val	Phe	Asp	His	Lys	Gly	Gly	Ala	Asp	Gly				
607				100					105					110						
609	acg	gaa	tgg	gtg	gac	gcc	gtc	gaa	gtc	aat	ccg	tcc	gac	cgc	aac	caa				384
610	Thr	Glu	Trp	Val	Asp	Ala	Val	Glu	Val	Asn	Pro	Ser	Asp	Arg	Asn	Gln				
611			115					120					125							
613	gaa	atc	tcg	ggc	acc	tat	caa	atc	caa	gca	tgg	acg	aaa	ttt	gat	ttt				432
614	Glu	Ile	Ser	Gly	Thr	Tyr	Gln	Ile	Gln	Ala	Trp	Thr	Lys	Phe	Asp	Phe				
615		130					135					140								
617	ccc	ggg	cgg	ggc	aac	acc	tac	tcc	agc	ttt	aag	tgg	cgc	tgg	tac	cat				480
618	Pro	Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Ser	Phe	Lys	Trp	Arg	Trp	Tyr	His				
619	145					150					155					160				
621	ttt	gac	ggc	gtt	gat	tgg	gac	gaa	agc	cga	aaa	ttg	agc	cgc	att	tac				528
622	Phe	Asp	Gly	Val	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Ser	Arg	Ile	Tyr				
623					165					170					175					
625	aaa	ttc	cgc	ggc	atc	ggc	aaa	gcg	tgg	gat	tgg	gaa	gta	gac	acg	gaa				576
626	Lys	Phe	Arg	Gly	Ile	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp	Thr	Glu				
627				180																

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Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\07152002\I925576B.raw

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649 ttg cac aat tac att acg aaa aca gac gga acg atg tct ttg ttt gat      864
650 Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp
651      275      280      285
653 gcc ccg tta cac aac aaa ttt tat acc gct tcc aaa tca ggg ggc gca      912
654 Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala
655      290      295      300
657 ttt gat atg cgc acg tta atg acc aat act ctc atg aaa gat caa ccg      960
658 Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
659 305      310      315      320
661 aca ttg gcc gtc acc ttc gtt gat aat cat gac acc gaa ccc ggc caa      1008
662 Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
663      325      330      335
665 gcg ctg cag tca tgg gtc gac cca tgg ttc aaa ccg ttg gct tac gcc      1056
666 Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
667      340      345      350
669 ttt att cta act cgg cag gaa gga tac ccg tgc gtc ttt tat ggt gac      1104
670 Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
671      355      360      365
673 tat tat ggc att cca caa tat aac att cct tcg ctg aaa agc aaa atc      1152
674 Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
675      370      375      380
677 gat ccg ctc ctc atc gcg cgc agg gat tat gct tac gga acg caa cat      1200
678 Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
679 385      390      395      400
681 gat tat ctt gat cac tcc gac atc atc ggg tgg aca agg gaa ggg ggc      1248
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W--> 684 <110> APPLICANT: Andersen, Carsten
W--> 684 <110> APPLICANT: Andersen, Carsten
W--> 688 <120> TITLE OF INVENTION: Amylase Variants
W--> 688 <120> TITLE OF INVENTION: Amylase Variants
W--> 690 <130> FILE REFERENCE: 10004.204-US
W--> 690 <130> FILE REFERENCE: 10004.204-US
W--> 692 <160> NUMBER OF SEQ ID NOS: 20
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W--> 694 <170> SOFTWARE: PatentIn version 3.1
696 <210> SEQ ID NO: 1
697 <211> LENGTH: 1455
698 <212> TYPE: DNA
699 <213> ORGANISM: Bacillus sp.
701 <220> FEATURE:
702 <221> NAME/KEY: CDS
703 <222> LOCATION: (1)..(1455)
704 <223> OTHER INFORMATION: SP690
707 <400> SEQUENCE: 1
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709 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
710 1      5      10      15
712 ttg cca aat gac ggg aat cat tgg aac agg ttg agg gat gac gca gct      96
713 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala

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SEQUENCE LISTING

*Remove
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Input Set : A:\PTOMS.txt

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714	20	25	30	
716	aac tta aag agt aaa ggg ata aca gct gta tgg atc cca cct gca tgg	144		
717	Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp			
718	35 40 45			
720	aag ggg act tcc cag aat gat gta ggt tat gga gcc tat gat tta tat	192		
721	Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr			
722	50 55 60			
724	gat ctt gga gag ttt aac cag aag ggg acg gtt cgt aca aaa tat gga	240		
725	Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly			
726	65 70 75 80			
728	aca cgc aac cag cta cag gct gcg gtg acc tct tta aaa aat aac ggc	288		
729	Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly			
730	85 90 95			
732	att cag gta tat ggt gat gtc gtc atg aat cat aaa ggt gga gca gat	336		
733	Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp			
734	100 105 110			
736	ggt acg gaa att gta aat gcg gta gaa gtg aat cgg agc aac cga aac	384		
737	Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn			
738	115 120 125			
740	cag gaa acc tca gga gag tat gca ata gaa gcg tgg aca aag ttt gat	432		
741	Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp			
742	130 135 140			
744	ttt cct gga aga gga aat aac cat tcc agc ttt aag tgg cgc tgg tat	480		
745	Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr			
746	145 150 155 160			
748	cat ttt gat ggg aca gat tgg gat cag tca cgc cag ctt caa aac aaa	528		
749	His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys			
750	165 170 175			
752	ata tat aaa ttc agg gga aca ggc aag gcc tgg gac tgg gaa gtc gat	576		
753	Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp			
754	180 185 190			
756	aca gag aat ggc aac tat gac tat ctt atg tat gca gac gtg gat atg	624		
757	Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met			
758	195 200 205			
760	gat cac cca gaa gta ata cat gaa ctt aga aac tgg gga gtg tgg tat	672		
761	Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr			
762	210 215 220			
764	acg aat aca ctg aac ctt gat gga ttt aga ata gat gca gtg aaa cat	720		
765	Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His			
766	225 230 235 240			
768	ata aaa tat agc ttt acg aga gat tgg ctt aca cat gtg cgt aac acc	768		
769	Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr			
770	245 250 255			
772	aca ggt aaa cca atg ttt gca gtg gct gag ttt tgg aaa aat gac ctt	816		
773	Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Tyr Ile Thr Lys Thr Asp			
W--> 774	Gly Thr Met Ser Leu Phe Asp			
W--> 775	275 280 285			
778	Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala			
W--> 779	290 295 300			

*remove
repeated
material*

RAW SEQUENCE LISTING

DATE: 07/15/2002

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Input Set : A:\PTOMS.txt

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      782 Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
W--> 783 305                310                315                320
      786 Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
W--> 787                325                330                335
      790 Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
W--> 791                340                345                350
      794 Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
W--> 795                355                360                365
      798 Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
W--> 799                370                375                380
      802 Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
W--> 803 385                390                395                400
      806 Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly
W--> 807                405                410                415
      810 Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
W--> 811                420                425                430
      814 Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
W--> 815                435                440                445
      818 Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
W--> 819                450                455                460
      822 Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
W--> 823 465                470                475                480
      826 Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr
W--> 827                485                490                495
      830 Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
W--> 831                500                505                510
      834 Ala Trp Pro
E--> 835                515
E--> 838 <210> SEQ ID NO: 7

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*remove
repeated
material*

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/925,576B

DATE: 07/15/2002
TIME: 09:11:13

Input Set : A:\PTOMS.txt
Output Set: N:\CRF3\07152002\I925576B.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 396

Skipped Sequences(NEW RULES):

Sequence(s) missing. If intentional, please use the following format for each skipped sequence.

<210> sequence id number

<400> sequence id number

000

Seq#:2,3,2,3,4,5,6

VERIFICATION SUMMARY

DATE: 07/15/2002

PATENT APPLICATION: US/09/925,576B

TIME: 09:11:13

Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\07152002\I925576B.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:305 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:305 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:305 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1455 Found:144 SEQ:3
L:307 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:307 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:311 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:311 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:313 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:313 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:315 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:315 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:317 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:396 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:397 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:397 M:254 E: No. of Bases conflict, LENGTH:Input:1056 Counted:834 SEQ:1
L:399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:419 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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L:431 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:435 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1455 Found:1233 SEQ:1
L:438 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 2 thru 3
L:682 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:682 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1548 Found:1248 SEQ:5
L:684 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:684 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:688 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:688 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:690 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:690 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:692 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:692 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:694 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:774 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:775 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:779 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:783 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:787 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:791 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:795 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

VERIFICATION SUMMARY

DATE: 07/15/2002

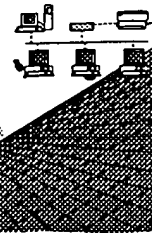
PATENT APPLICATION: US/09/925,576B

TIME: 09:11:13

Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\07152002\I925576B.raw

L:799 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:803 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:807 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:811 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:815 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:819 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:823 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:827 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:831 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:835 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:835 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1455 Found:816 SEQ:1
L:838 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 2 thru 6
L:692 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (20) Counted (21)



Q570
0606

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